Correction to: Germinal Immunogenetics predict treatment outcome for PD-1/PD-L1 checkpoint inhibitors

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Corrections are needed to the original version of this article. The in-text citations of tables and figures in the section “*results*” are not in sequential order. Moreover in section “*results*” (Associations between treatment outcome and SNPs), the reader should read “Almost half the patients (43.5%, N = 41) were in the low-risk group” and not “Almost half the patients (43.5%, N = 53) were in the low-risk group”.

The authors apologize for corrections and further state that changes to the text and the sequence of figures and tables does not affect the overall outcome of the study.

- Table 3 should show the univariate analysis for the 163 SNPs according to treatment outcome. Instead in the original paper it is presented in Table 4. For rs13900 the alleles associated with recessive model are “C/C or C/T” and not “C/C or T/T” as written in the table.

- Table 4 should show the univariate analysis for the 163 SNPs according to toxicity, instead in the original paper it is presented in Table 3.
- Table 5 should respectively show the weight of each SNP for multivariate predictive model according to treatment outcome and toxicity. Moreover in “*Treatment outcome*” the modality for rs13900 is T/T and not C/T.
- Table 6 should show the classification of patients based on risk group and risk evaluation of each group. For a better reading of table, the results “*Treatment Outcome*” and “*Toxicity*” have been reversed.
- Figure 1a should show the performance of the treatment predictive model, instead in the original paper it is presented in the Fig. 1b
- Figure 1b should show the performance of the toxicity predictive model, instead in the original paper it is presented in the Fig. 1a

The online version of the original article can be found at <https://doi.org/10.1007/s10637-019-00845-w>

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Table 3 Univariate analysis for the 163 SNPs according to treatment outcome

Variable SNPs	Model	Genotype	RC or RP	SD or PR	OR	CI95%	<i>P</i> value
rs1799983 (NOS3)	Dominant	G/G	13 (26.5)	22 (48.9)	1	Referent	0.026
		G/T or T/T	36 (73.5)	23 (51.1)	0.37	[0.15–0.91]	
rs4845618 (IL6R)	Dominant	T/T	14 (28.6)	23 (51.1)	1	Referent	0.027
		G/T or G/G	35 (71.4)	22 (48.9)	0.38	[0.16–0.91]	
rs3212227 (IL12B)	Dominant	T/T	23 (46.9)	31 (68.9)	1	Referent	0.033
		G/T or G/G	26 (53.1)	14 (31.1)	0.39	[0.16–0.94]	
rs419598 (IL1RN)	Dominant	T/T	33 (67.3)	18 (40)	1	Referent	0.008
		C/T or C/C	16 (32.7)	27 (60)	3.09	[1.30–7.32]	
rs2280964 (CXCR3)	Dominant	C/C	33 (67.3)	39 (86.7)	1	Referent	0.031
		C/T or T/T	16 (32.7)	6 (13.3)	0.31	[0.10–0.92]	
rs13900 (CCL2)	Recessive	C/C or C/T	49 (100)	41 (91.1)	1	Referent	0.048*
		T/T	0 (0)	4 (8.9)	–	[– –]	
rs4586 (CCL2)	Recessive	T/T or C/T	47 (95.9)	37 (82.2)	1	Referent	0.047
		C/C	2 (4.1)	8 (17.8)	5.08	[0.98–26.25]	
rs1024611 (CCL2)	Recessive	A/A or A/G	49 (100)	41 (91.1)	1	Referent	0.048*
		G/G	0 (0)	4 (8.9)	–	[– –]	
Patients and tumor characteristics							
Age			65.3 (10.3)	67.4 (9.5)	1.02	[0.98–1.066]	0.31
Gender		Female	18 (42.9)	22 (48.9)	1	Referent	0.419
		Male	28 (57.1)	23 (51.1)	1.43	[0.589–3.466]	
Tabaco		No	12 (24.5)	12 (26.7)	1	Referent	0.809
		Yes	37 (75.5)	33 (73.3)	0.89	[0.346–2.298]	
Histology		HNSCC	6 (12.2)	7 (15.6)	1	Referent	0.806
		NSCLC	24 (49)	24 (53.3)	0.85	[0.24–3.00]	
		Melanoma	9 (18.4)	3 (6.7)	0.28	[0.05–1.62]	
		Renal cell carcinoma	6 (12.2)	8 (17.8)	1.14	[0.24–5.38]	
		Other	4 (8.2)	3 (6.7)	0.64	[0.09–4.25]	
Radiotherapy		No	18 (36.7)	12 (26.7)	1	Referent	0.297
		Yes	31 (53.1)	33 (73.3)	1.59	[0.65–3.92]	
Number of lines before recurrence		0–1	31 (63.3)	32 (71.1)	1	Referent	0.419
		≥2	18 (36.7)	13 (28.9)	0.7	[0.28 - 1.69]	

* OR not calculable replaced by Fisher's test;

Table 4 Univariate analysis for the 163 SNPs according to toxicity.

Variable SNPs	Model	Genotype	IrAe < 3	IrAe ≥ 3	OR	CI95%	<i>p</i> value
rs246079 (UNG)	Dominant	A/A	21 (26.6)	12 (80)	1	Referent	
		A/G or G/G	58 (73.4)	3 (20)	0.09	[0.02–0.36]	< 0.001
rs10964859 (IFNW1)	Recessive	C/C or C/G	73 (92.4)	10 (66.7)	1	Referent	
		G/G	6 (7.6)	5 (33.3)	6.08	[1.52–24.33]	0.014
rs4143815 (PD-L1)	Recessive	G/G or G/C	73 (92.4)	9 (60)	1	Referent	
		C/C	6 (7.6)	6 (40)	8.11	[2.09–31.40]	0.003
rs12979860 (IFNL4)	Recessive	C/C or C/T	67 (84.8)	9 (60)	1	Referent	
		T/T	12 (15.2)	6 (40)	3.72	[1.09–12.68]	0.036
rs3087243 (CTLA4)	Recessive	A/A or A/G	62 (78.5)	8 (53.3)	1	Referent	
		G/G	17 (21.5)	7 (46.7)	3.19	[1.01–10.27]	0.048
rs11571302 (CTLA4)	Recessive	T/T or G/T	65 (82.3)	8 (53.3)	1	Referent	
		G/G	14 (17.7)	7 (46.7)	4.06	[1.23–13.38]	0.018
rs7565213 (CTLA4)	Recessive	A/A or A/G	64 (81)	8 (53.3)	1	Referent	
		G/G	15 (19)	7 (46.7)	3.73	[1.14–12.19]	0.026
Patients and tumor characteristics							
Age			65.5 (10)	70.5 (8.4)	1.062	[0.99–1.13]	0.075
Gender		Female	25 (31.6)	6 (40)	1	Referent	
		Male	54 (68.4)	9 (60)	0.69	[0.21–2.21]	0.53
Tobacco		No	20 (25.3)	4 (26.7)	1	Referent	
		Yes	59 (74.7)	11 (73.3)	0.93	[0.26–3.34]	0.91
Histology		HNSCC*	11 (13.9)	2 (13.3)	1	Referent	
		NSCLC**	41 (51.9)	7 (46.7)	0.94	[0.16–5.36]	0.94
		Melanoma	11 (13.9)	1 (6.7)	0.50	[0.03–6.69]	0.59
		Renal cell carcinoma	11 (13.9)	3 (20)	1.50	[0.20–11.25]	0.68
		Other	5 (6.3)	2 (13.3)	2.20	[0.22–21.33]	0.48
Radiotherapy		No	23 (29.1)	7 (46.7)	1	Referent	
		Yes	56 (70.9)	8 (53.3)	0.47	[0.14–1.48]	0.18
Number of lines before recurrence		0–1	53 (67.1)	10 (66.7)	1	Referent	
		≥2	26 (32.9)	5 (33.3)	1.01	[0.30–3.37]	0.97

* HNSCC: Head and neck squamous cell carcinoma; ** NSCLC: non-small cell lung carcinoma

Table 5 Weight of each variable for multivariate predictive model

rs ID (Gene)	Chr	Ancestral allele	Minor Allele Frequency	Modality	Weight
<i>Treatment outcome</i>					
rs13900 (CCL2)	17	C	0.5	T/T	347
rs1799983 (NOS3)	7	G	0.4	G/G	133
rs3212227 (IL12B)	5	T	0.5	T/T	133
rs419598 (IL1RN)	2	T	0.42	C/T or C/C	133
rs2280964 (CXCR3)	X	C	0.49	C/C	119
rs4845618 (IL6R)	1	G	0.49	T/T	102
rs4586 (CCL2)	17	C	0.46	C/C	32
<i>Toxicity</i>					
rs10964859 (IFNW1)	9	C	0.37	G/G	243
rs246079 (UNG)	12	G	0.41	A/A	243
rs3087243 (CTLA4)	2	G	0.45	G/G	187
rs4143815 (PDL-1)	9	G	0.33	C/C	175
rs12979860 (IFNL4)	19	T	0.32	T/T	152

Table 6 Classification of patients based on risk group and risk evaluation of each group

<i>Treatment Outcome</i>					
Risk group	Total n (%)	RC or PR	SD or PD	Odds Ratio (CI 95%)	p
Low risk	41 (43.5%)	33 (80.5%)	8 (19.5%)	1.0 referent	0.006
Intermediate risk	27 (29%)	13 (48%)	14 (52%)	4.42 [1.48–13.37]	
High risk	26 (27.5%)	3 (11.5%)	23 (88.5%)	31.62 [7.36–135.91]	<0.001
<i>Toxicity</i>					
		No IrAE	IrAE		
Low risk	70 (74.5%)	67 (95.7%)	3 (4.3%)	1.0 referent	<0.001
High risk	24 (25.5%)	12 (50%)	12 (50%)	22.33 [5.31–93.87]	

a Treatment outcome **b** Toxicity

Fig. 1 ROC curves representation and AUC estimation for predictive model. **a** Treatment outcome, **b** Toxicity

Fig. 2 Patients distribution in the different risk groups according on the predictive model. **a** Treatment outcome, **b** Toxicity

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